



OIEP

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/865,363

DATE: 01/23/2002  
 TIME: 09:53:48

Input Set : N:\Crf3\RULE60\09865363.raw.txt  
 Output Set: N:\CRF3\01232002\I865363.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Anderson, Dirk M.  
 6 Galibert, Laurent  
 7 Maraskovsky, Eugene  
 9 (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
 11 (iii) NUMBER OF SEQUENCES: 19  
 13 (iv) CORRESPONDENCE ADDRESS:  
 14 (A) ADDRESSEE: Immunex Corporation, Law Department  
 15 (B) STREET: 51 University Street  
 16 (C) CITY: Seattle  
 17 (D) STATE: WA  
 18 (E) COUNTRY: USA  
 19 (F) ZIP: 98101

ENTERED

## 21 (v) COMPUTER READABLE FORM:

- 22 (A) MEDIUM TYPE: Floppy disk  
 23 (B) COMPUTER: Apple Power Macintosh  
 24 (C) OPERATING SYSTEM: Apple Operating System 7.5.5  
 25 (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

## 27 (vi) CURRENT APPLICATION DATA:

- C--> 28 (A) APPLICATION NUMBER: US/09/865,363  
 C--> 29 (B) FILING DATE: 25-May-2001  
 45 (C) CLASSIFICATION:

## 42 (vii) PRIOR APPLICATION DATA:

- 33 (A) APPLICATION NUMBER: 08/995,659  
 34 (B) FILING DATE:  
 38 (A) APPLICATION NUMBER: USSN 08/813,509  
 39 (B) FILING DATE: 07 MARCH 1997  
 43 (A) APPLICATION NUMBER: USSN 08/772,330  
 44 (B) FILING DATE: 23 DECEMBER 1996

## 47 (viii) ATTORNEY/AGENT INFORMATION:

- 48 (A) NAME: Perkins, Patricia Anne  
 49 (B) REGISTRATION NUMBER: 34,693  
 50 (C) REFERENCE/DOCKET NUMBER: 2852-A

## 52 (ix) TELECOMMUNICATION INFORMATION:

- 53 (A) TELEPHONE: (206)587-0430  
 54 (B) TELEFAX: (206)233-0644

## 57 (2) INFORMATION FOR SEQ ID NO: 1:

## 59 (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 3115 base pairs  
 61 (B) TYPE: nucleic acid  
 62 (C) STRANDEDNESS: single  
 63 (D) TOPOLOGY: linear

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65      (ii) MOLECULE TYPE: cDNA
67      (iii) HYPOTHETICAL: NO
69      (iv) ANTI-SENSE: NO
71      (vi) ORIGINAL SOURCE:
72          (A) ORGANISM: HOMO SAPIENS
74      (vii) IMMEDIATE SOURCE:
75          (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
76          (B) CLONE: 9D-8A
78      (ix) FEATURE:
79          (A) NAME/KEY: CDS
80          (B) LOCATION: 93..1868
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
85      GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG      60
87      GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT      113
88                                     Val Ala Leu Gln Ile Ala Pro
89                                     1           5
91      CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC      161
92      Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
93          10           15           20
95      AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT      209
96      Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
97          25           30           35
99      GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG      257
100     Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
101     40           45           50           55
103     AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG      305
104     Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
105           60           65           70
107     GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC      353
108     Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
109           75           80           85
111     GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC      401
112     Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
113           90           95           100
115     CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG      449
116     Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
117           105           110           115
119     CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT      497
120     Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
121     120           125           130           135
123     GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC      545
124     Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
125           140           145           150
127     TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG      593
128     Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
129           155           160           165
131     GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT      641
132     Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
133           170           175           180

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135	GTT	TAC	TTG	CCC	GGT	TTA	ATA	ATT	CTG	CTT	CTC	TTC	GCG	TCT	GTG	GCC	689
136	Val	Tyr	Leu	Pro	Gly	Leu	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala	
137	185						190					195					
139	CTG	GTG	GCT	GCC	ATC	ATC	TTT	GGC	GTT	TGC	TAT	AGG	AAA	AAA	GGG	AAA	737
140	Leu	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys	
141	200					205					210					215	
143	GCA	CTC	ACA	GCT	AAT	TTG	TGG	CAC	TGG	ATC	AAT	GAG	GCT	TGT	GGC	CGC	785
144	Ala	Leu	Thr	Ala	Asn	Leu	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg	
145					220					225					230		
147	CTA	AGT	GGA	GAT	AAG	GAG	TCC	TCA	GGT	GAC	AGT	TGT	GTC	AGT	ACA	CAC	833
148	Leu	Ser	Gly	Asp	Lys	Glu	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His	
149				235					240					245			
151	ACG	GCA	AAC	TTT	GGT	CAG	CAG	GGA	GCA	TGT	GAA	GGT	GTC	TTA	CTG	CTG	881
152	Thr	Ala	Asn	Phe	Gly	Gln	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	
153			250					255					260				
155	ACT	CTG	GAG	GAG	AAG	ACA	TTT	CCA	GAA	GAT	ATG	TGC	TAC	CCA	GAT	CAA	929
156	Thr	Leu	Glu	Glu	Lys	Thr	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	
157		265					270				275						
159	GGT	GGT	GTC	TGT	CAG	GGC	ACG	TGT	GTA	GGA	GGT	CCC	TAC	GCA	CAA		977
160	Gly	Gly	Val	Cys	Gln	Gly	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	
161	280					285					290					295	
163	GGC	GAA	GAT	GCC	AGG	ATG	CTC	TCA	TTG	GTC	AGC	AAG	ACC	GAG	ATA	GAG	1025
164	Gly	Glu	Asp	Ala	Arg	Met	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	
165				300						305					310		
167	GAA	GAC	AGC	TTC	AGA	CAG	ATG	CCC	ACA	GAA	GAT	GAA	TAC	ATG	GAC	AGG	1073
168	Glu	Asp	Ser	Phe	Arg	Gln	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	
169			315						320					325			
171	CCC	TCC	CAG	CCC	ACA	GAC	CAG	TTA	CTG	TTC	CTC	ACT	GAG	CCT	GGA	AGC	1121
172	Pro	Ser	Gln	Pro	Thr	Asp	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	
173			330				335						340				
175	AAA	TCC	ACA	CCT	CCT	TTC	TCT	GAA	CCC	CTG	GAG	GTG	GGG	GAG	AAT	GAC	1169
176	Lys	Ser	Thr	Pro	Pro	Phe	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	
177		345					350					355					
179	AGT	TTA	AGC	CAG	TGC	TTC	ACG	GGG	ACA	CAG	AGC	ACA	GTG	GGT	TCA	GAA	1217
180	Ser	Leu	Ser	Gln	Cys	Phe	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	
181	360					365					370					375	
183	AGC	TGC	AAC	TGC	ACT	GAG	CCC	CTG	TGC	AGG	ACT	GAT	TGG	ACT	CCC	ATG	1265
184	Ser	Cys	Asn	Cys	Thr	Glu	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	
185					380					385					390		
187	TCC	TCT	GAA	AAC	TAC	TTG	CAA	AAA	GAG	GTG	GAC	AGT	GGC	CAT	TGC	CCG	1313
188	Ser	Ser	Glu	Asn	Tyr	Leu	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	
189			395						400					405			
191	CAC	TGG	GCA	GCC	AGC	CCC	AGC	CCC	AAC	TGG	GCA	GAT	GTC	TGC	ACA	GGC	1361
192	His	Trp	Ala	Ala	Ser	Pro	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	
193			410					415					420				
195	TGC	CGG	AAC	CCT	CCT	GGG	GAG	GAC	TGT	GAA	CCC	CTC	GTG	GGT	TCC	CCA	1409
196	Cys	Arg	Asn	Pro	Pro	Gly	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	
197		425					430				435						
199	AAA	CGT	GGA	CCC	TTG	CCC	CAG	TGC	GCC	TAT	GGC	ATG	GGC	CTT	CCC	CCT	1457

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200	Lys	Arg	Gly	Pro	Leu	Pro	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	
201	440					445					450					455	
203	GAA	GAA	GAA	GCC	AGC	AGG	ACG	GAG	GCC	AGA	GAC	CAG	CCC	GAG	GAT	GGG	1505
204	Glu	Glu	Glu	Ala	Ser	Arg	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	
205					460					465					470		
207	GCT	GAT	GGG	AGG	CTC	CCA	AGC	TCA	GCG	AGG	GCA	GGT	GCC	GGG	TCT	GGA	1553
208	Ala	Asp	Gly	Arg	Leu	Pro	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	
209					475				480					485			
211	AGC	TCC	CCT	GGT	GGC	CAG	TCC	CCT	GCA	TCT	GGA	AAT	GTG	ACT	GGA	AAC	1601
212	Ser	Ser	Pro	Gly	Gly	Gln	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	
213			490					495					500				
215	AGT	AAC	TCC	ACG	TTC	ATC	TCC	AGC	GGG	CAG	GTG	ATG	AAC	TTC	AAG	GGC	1649
216	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	
217		505					510				515						
219	GAC	ATC	ATC	GTG	GTC	TAC	GTC	AGC	CAG	ACC	TCG	CAG	GAG	GGC	GCG	GCG	1697
220	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	
221	520					525					530					535	
223	GCG	GCT	GCG	GAG	CCC	ATG	GGC	CGC	CCG	GTG	CAG	GAG	GAG	ACC	CTG	GCG	1745
224	Ala	Ala	Ala	Glu	Pro	Met	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	
225					540					545					550		
227	CGC	CGA	GAC	TCC	TTC	GCG	GGG	AAC	GGC	CCG	CGC	TTC	CCG	GAC	CCG	TGC	1793
228	Arg	Arg	Asp	Ser	Phe	Ala	Gly	Asn	Gly	Pro	Arg	Phe	Pro	Asp	Pro	Cys	
229			555						560					565			
231	GGC	GGC	CCC	GAG	GGG	CTG	CGG	GAG	CCG	GAG	AAG	GCC	TCG	AGG	CCG	GTG	1841
232	Gly	Gly	Pro	Glu	Gly	Leu	Arg	Glu	Pro	Glu	Lys	Ala	Ser	Arg	Pro	Val	
233			570					575					580				
235	CAG	GAG	CAA	GGC	GGG	GCC	AAG	GCT	TGA	GCGCCCCCA	TGGCTGGGAG						1888
236	Gln	Glu	Gln	Gly	Gly	Ala	Lys	Ala									
237		585					590										
239	CCCGAAGCTC	GGAGCCAGGG	CTCGCGAGGG	CAGCACCGCA	GCCTCTGCCC	CAGCCCCGGC											1948
241	CACCCAGGGA	TCGATCGGTA	CAGTCGAGGA	AGACCACCCG	GCATTCTCTG	CCCACCTTGC											2008
243	CTTCCAGGAA	ATGGGCTTTT	CAGGAAGTGA	ATTGATGAGG	ACTGTCCCCA	TGCCCACGGA											2068
245	TGCTCAGCAG	CCCGCCGCAC	TGGGGCAGAT	GTCTCCCCTG	CCACTCCTCA	AACTCGCAGC											2128
247	AGTAATTTGT	GGCACTATGA	CAGCTATTTT	TATGACTATC	CTGTTCTGTG	GGGGGGGGGT											2188
249	CTATGTTTTT	CCCCCATATT	TGTATTCCTT	TTCTAACTT	TTCTTGATAT	CTTTCTCTCC											2248
251	TCTTTTTTAA	TGTAAAGGTT	TTCTCAAAAA	TTCTCCTAAA	GGTGAGGGTC	TCTTTCTTTT											2308
253	CTCTTTTCTT	TTTTTTTTTC	TTTTTTTGGC	AACCTGGCTC	TGGCCCAGGC	TAGAGTGCAG											2368
255	TGGTGCATT	ATAGCCCGGT	GCAGCCTCTA	ACTCCTGGGC	TCAAGCAATC	CAAGTGATCC											2428
257	TCCACCTCA	ACCTTCGGAG	TAGCTGGGAT	CACAGCTGCA	GGCCACGCCC	AGCTTCCTCC											2488
259	CCCCGACTCC	CCCCCCCCAG	AGACACGGTC	CCACCATGTT	ACCCAGCCTG	GTCTCAAAC											2548
261	CCCCAGCTAA	AGCAGTCCTC	CAGCCTCGGC	CTCCCAAAGT	ACTGGGATTA	CAGGCGTGAG											2608
263	CCCCACGCT	GGCCTGCTTT	ACGTATTTTC	TTTTGTGCCC	CTGCTCACAG	TGTTTTAGAG											2668
265	ATGGCTTTCC	CAGTGTGTGT	TCATTGTAAA	CACTTTGGG	AAAGGGCTAA	ACATGTGAGG											2728
267	CCTGGAGATA	GTTGCTAAGT	TGCTAGGAAC	ATGTGGTGGG	ACTTTCATAT	TCTGAAAAAT											2788
269	GTTCTATATT	CTCATTTTTT	TAAAAGAAAG	AAAAAAGGAA	ACCCGATTTA	TTTCTCCTGA											2848
271	ATCTTTTTTAA	GTTTGTGTCT	TTCTTAAGC	AGAACTAAGC	TCAGTATGTG	ACCTTACCCG											2908
273	CTAGGTGGTT	AATTTATCCA	TGCTGGCAGA	GGCACTCAGG	TACTTGGTAA	GCAAATTTCT											2968
275	AAAACCTCAA	GTTGCTGCAG	CTTGGCATTC	TTCTTATTCT	AGAGGTCTCT	CTGGAAAAGA											3028
277	TGGAGAAAAT	GAACAGGACA	TGGGGCTCCT	GGAAAGAAAG	GGCCCCGGGA	GTTCAAGGAA											3088

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279 GAATAAAGTT GAAATTTTAA AAAAAAA 3115

282 (2) INFORMATION FOR SEQ ID NO: 2:

284 (i) SEQUENCE CHARACTERISTICS:

285 (A) LENGTH: 591 amino acids

286 (B) TYPE: amino acid

287 (D) TOPOLOGY: linear

289 (ii) MOLECULE TYPE: protein

291 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

293 Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu  
294 1 5 10 15  
296 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser  
297 20 25 30  
299 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro  
300 35 40 45  
302 Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His  
303 50 55 60  
305 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn  
306 65 70 75 80  
308 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser  
309 85 90 95  
311 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu  
312 100 105 110  
314 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro  
315 115 120 125  
317 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys  
318 130 135 140  
320 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His  
321 145 150 155 160  
323 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg  
324 165 170 175  
326 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu  
327 180 185 190  
329 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val  
330 195 200 205  
332 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp  
333 210 215 220  
335 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly  
336 225 230 235 240  
338 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala  
339 245 250 255  
341 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu  
342 260 265 270  
344 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val  
345 275 280 285  
347 Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu  
348 290 295 300  
350 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr  
351 305 310 315 320  
353 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09865363.raw.txt

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:445 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:449 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:459 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:473 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:477 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:487 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:491 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:501 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
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L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:515 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:524 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:528 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:533 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:537 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:551 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:555 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:560 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

L:566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3